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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 16:19:50 ; Search time 2330 Seconds

(without alignments)  
1357.958 Million cell updates/sec

Title: US-10-658-093-19

Perfect score: 73  
Sequence: 1 aacgttattatgcttttta.....tattttattatttttttt 73

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenBank1:\*  
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2: gb\_htg:\*  
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11: gb\_sts:\*  
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14: gb\_vl:\*  
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40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	* Match	Length	DB	ID	Description
C 1	73	100.0	242	6	AX340922	AX340922 Sequence
C 2	73	100.0	245	6	AX587935	AX587935 Sequence
C 3	73	100.0	265	12	SYNINFOSP	M28858 Synthetic (
C 4	73	100.0	477	6	AX774881	AX774881 Sequence
C 5	73	100.0	1918	9	AK097379	AK097379 Homo sapi
6	73	100.0	2084	6	AX587848	AX587848 Sequence
7	73	100.0	2103	6	AX014320	AX014320 Sequence
8	73	100.0	2103	6	BD222199	BD222199 Human nuc
9	73	100.0	2121	9	HSM807248	BX647104 Homo sapi
10	73	100.0	3565	6	196207	196207 Sequence 44
11	73	100.0	3565	6	AX330284	AX330284 Sequence
12	73	100.0	3565	6	AX36394	AX36394 Sequence
13	73	100.0	3565	6	AX663638	AX663638 Sequence
14	73	100.0	3565	9	HSCFOS	V01512 Human cellu
15	73	100.0	4200	4	SSC132510	AJ132510 Sus scrof
16	73	100.0	5897	9	AX212879	AJ132510 Sus scrof
17	73	100.0	6210	6	AX663628	AY122879 Homo sapi
18	73	100.0	6210	9	HOMFOS	AX663628 Sequence
19	73	100.0	135050	2	AC118536	K00650 Human fos p
20	73	100.0	140332	2	AC118538	AC118536 Canis fam
21	73	100.0	168802	2	AC147196	AC118538 Felle cat
22	73	100.0	174298	2	AC120514	AC147196 Sus scrof
23	73	100.0	181848	9	CNS07YOR	AC120514 Bos tauru
24	73	100.0	188938	2	AC119064	AL691403 Human chr
25	73	100.0	195254	2	AC117934	AC119064 Sus scrof
26	73	100.0	197796	2	AC117932	AC117934 Papio anu
27	73	100.0	202267	9	DJ293M10	AC117932 Papio anu
28	73	100.0	207930	2	AC120203	AF111167 Homo sapi
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30	71.4	97.8	402	6	AR272842	AF540379 Felle cat
31	71.4	97.8	402	6	AR272850	AR272842 Sequence
32	71.4	97.8	402	6	AR276423	AR272850 Sequence
33	71.4	97.8	402	6	AR276431	AR276423 Sequence
34	71.4	97.8	402	6	AR406698	AR276431 Sequence
35	71.4	97.8	402	6	AR406706	AR406698 Sequence
36	71.4	97.8	402	6	AX062944	AR406706 Sequence
37	71.4	97.8	402	6	AX062952	AX062944 Sequence
38	71.4	97.8	402	6	AX367861	AX062952 Sequence
39	71.4	97.8	402	6	AX367869	AX367861 Sequence
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# ALIGNMENTS

RESULT 1  
AX340922/c  
LOCUS AX340922  
DEFINITION Sequence 1169 from Patent WO0196388.  
ACCESSION AX340922  
VERSION AX340922.1 GI:18136904  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
Jiang Y., Harlocker, S.L. and Secrist, H.  
TITLE Compositions and methods for the therapy and diagnosis of colon cancer

JOURNAL Patent: WO 0196388-A 1169 20-DEC-2001;  
CORIXA CORPORATION (US)  
Location/Qualifiers

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source  
1. .242  
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/db\_xref="taxon:9606"

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Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATTCCTCAGATATTATATTTT 60  
DB 190 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATTCCTCAGATATTATATTTT 131  
CY 61 ATTTATTTT 73  
DB 130 ATTTATTTT 118

RESULT 2  
AX587935/c  
LOCUS AX587935 245 bp DNA linear PAT 10-JAN-2003  
DEFINITION Sequence 405 from Patent WO0246467.  
ACCESSION AX587935  
VERSION AX587935.1 GI:27656605  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Bertucci, F., Houlgate, R., Birnbaum, D., Nguyen, C., Vicens, P. and Fert, V.  
TITLE Gene expression profiling of primary breast carcinomas using arrays of candidate genes  
JOURNAL Patent: WO 0246467-A 405 13-JUN-2002;  
Ipsogen (FR)  
Location/Qualifiers  
FEATURES  
source  
1. .245  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
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/note="5' terminal sequence. v-fos fbj murine osteosarcoma viral oncogene homolog (FOS) gene."

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Query Match 100.0%; Score 73; DB 6; Length 245;  
Best Local Similarity 100.0%; Pred. No. 0.00043;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATTCCTCAGATATTATATTTT 60  
DB 180 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATTCCTCAGATATTATATTTT 121  
CY 61 ATTTATTTT 73  
DB 120 ATTTATTTT 108

RESULT 3  
SYNINFOSP  
LOCUS SYNINFOSP 265 bp mRNA linear SYN 01-JUN-1994  
DEFINITION Synthetic (plasmid psolif 3 fos AU-) interferon(IFN)-beta-c-fos mRNA, 3'UTR.  
ACCESSION M28858  
VERSION M28858.1 GI:496260  
KEYWORDS interferon-beta; synthetic.  
SOURCE synthetic construct  
ORGANISM synthetic construct

REFERENCE  
AUTHORS Krivos, V., Martin, O., Shaw, G., Deschamps, J. and Huez, G.  
TITLE Translational blockade imposed by cytokine-derived UA-rich sequences  
JOURNAL Science 245 (4920), 852-855 (1989)  
MEDLINE 89368907  
PubMed 2672333  
COMMENT On Jun 4, 1994 this sequence version replaced gi:342034.  
FEATURES  
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1. .265  
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1. .265  
/note="IFN-beta-c-fos"

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Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATTCCTCAGATATTATATTTT 60  
DB 81 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATTCCTCAGATATTATATTTT 140  
CY 61 ATTTATTTT 73  
DB 141 ATTTATTTT 153

RESULT 4  
AX774881/c  
LOCUS AX774881 477 bp DNA linear PAT 09-JUL-2003  
DEFINITION Sequence 197 from Patent WO03038129.  
ACCESSION AX774881  
VERSION AX774881.1 GI:32486397  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Rapont, M.  
TITLE Methods for assessing and treating leukemia  
JOURNAL Patent: WO 03038129-A 197 08-MAY-2003;  
Ortho-Clinical Diagnostics, Inc. (US)  
Location/Qualifiers  
FEATURES  
source  
1. .477  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00036;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATTCCTCAGATATTATATTTT 60  
DB 189 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATTCCTCAGATATTATATTTT 130  
CY 61 ATTTATTTT 73  
DB 129 ATTTATTTT 117

RESULT 5  
AK097379  
LOCUS AK097379 1918 bp mRNA linear PRI 15-JUL-2002

DEFINITION Homo sapiens cDNA FLJ40060 fis. clone TCOLN2000236, highly similar to P55-C-FOS PROTO-ONCOGENE PROTEIN.

ACCESSION AK097379

VERSION AK097379.1 GI:21757114

KEYWORDS oligo cloning; file (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS 1 Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T., Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuma,N., Sato,K., Tanikawa,M., Yamazaki,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,U., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagaharti,K., Masuhio,Y., Nagai,K. and Isogai,T.

TITLE NED0 human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1918)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomc@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NED0 human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

Source

1..1918

/organism="Homo sapiens"

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/db\_xref="taxon:9606"

/clone="TCOLN2000236"

/tissue\_type="colon, tumor tissue"

/clone\_11b="TCOLN2"

/note="Cloning vector: pEM18FLJ3"

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Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATATTATTTT 60

DB 1737 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATATTATTTT 1796

QY 61 ATTTATTTT 73

DB 1797 ATTTATTTT 1809

LOCUS AX587848 2084 bp DNA linear PAT 10-JAN-2003

DEFINITION Sequence 318 from Patent WO246467.

ACCESSION AX587848

VERSION AX587848.1 GI:28212432

KEYWORDS

SOURCE

1 synthetic construct

2 synthetic construct

3 artificial sequences.

REFERENCE Bertucci,F., Houlgate,R., Birnbaum,D., Nguyen,C., Viens,P. and

AUTHORS Pert,V.

TITLE Gene expression profiling of primary breast carcinomas using arrays

JOURNAL of candidate genes

PATENT Patent: WO 0246467-A 318 13-JUN-2002;

IPSOGEN (FR)

FEATURES

Source

1..2084

/organism="synthetic construct"

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/note="primer"

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1..2084

/note="fos fpi murine osteosarcoma viral oncogene homolog (FOS) gene."

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Query Match 100.0%; Score 73; DB 6; Length 2084;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATATTATTTT 60

DB 1922 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATATTATTTT 1981

QY 61 ATTTATTTT 73

DB 1992 ATTTATTTT 1994

LOCUS AX014320 2103 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 28 from Patent WO9954353.

ACCESSION AX014320

VERSION AX014320.1 GI:10040674

KEYWORDS

SOURCE

1 Homo sapiens (human)

2 Homo sapiens

3 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 Schmitz,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilarsky,C.

TITLE Human nucleic acid sequences of normal uterus tissue

JOURNAL Patent: WO 9954353-A 28 28-OCT-1999;

SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METZGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)

FEATURES

Source

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/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

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Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATATTATTTT 60

DB 1878 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATATTATTTT 1937

QY 61 ATTTATTTT 73

DB 1938 ATTTATTTT 1950

LOCUS BD222199 2103 bp DNA linear PAT 17-JUL-2003

DEFINITION Human nucleic acid sequence originating in normal uterine tissue.

ACCESSION BD222199

VERSION BD222199.1 GI:33031969

KEYWORDS

UP 2002512017-A/28.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 2103)  
AUTHORS Specht, T., Hinzmann, B., Schmitt, A., Pilarsky, C., Dahl, E. and Rosenthal, A.  
TITLE Human nucleic acid sequence originating in normal uterine tissue  
JOURNAL Patent: JP 2002512017-A 28 23-APR-2002;  
COMMENT METAGEN GEBELTSCHAFT FUER GENOM FORSCHUNG MBH  
OS Homo sapiens (human)  
PN JP 2002512017-A/28  
PD 23-APR-2002 JP 2000544691  
PF 15-APR-1999 JP 2000544691  
PR 17-APR-1998 DE 198 17 946.4  
PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,  
PI EDGAR DAHL,  
PI ANDRE ROSENTHAL,  
PC C12N15/09,A61K38/00,A61K48/00,A61P35/00,C07K14/47,C07K16/18,  
PC C12N1/19,  
PC C12N1/21,C12N5/00,C12P21/08,C12Q1/68,G01N33/68,C12N15/00, PC  
A61K37/02,  
PC C12N5/00  
CC Human nucleic acid sequence originating in normal uterine CC  
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DB 1878 AACGTTTATGCTGTTTAAATTTATTTAATGATGATTCACAGATTTATTTATTTT 1937  
QY 61 ATTTATTTT 73  
DB 1938 ATTTATTTT 1950  
RESULT 9  
HSM807248 2121 bp mRNA linear PRI 30-AUG-2003  
LOCUS HSM807248  
DEFINITION Homo sapiens mRNA; cDNA DKFZp686J04124 (from clone DKFZp686J04124).  
ACCESSION BX647104  
VERSION BX647104.1 GI:34366132  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 2121)  
AUTHORS Mamula, J.; Butera, J.; Primates; Catarrhini; Homidae; Homo.  
TITLE 1 (bases 1 to 2121)  
JOURNAL Fodor, G., Han, M., and Wiemann, S.  
COMMENT Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amd, C., Osanger, A.,  
The German Human CDNA Consortium  
Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuberger, GERMANY  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by AGOWA (Berlin/Germany) within the CDNA sequencing  
consortium of the German Genome Project.  
This clone (DKFZp686J04124) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further

information about the clone and the sequencing project is available  
at <http://mips.gsf.de/proc/cdna/>.  
Location/Qualifiers  
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/issue\_type="human uterus"  
/clone\_lib="686 (synonym: h1ccc3). Vector pSport1\_Sfi; host  
DH10B; sites SfiIA + SfiIB"  
/dev\_stage="adult"  
2078..2083  
polyA\_signal  
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2102  
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DB 1921 AACGTTTATGCTGTTTAAATTTATTTAATGATGATTCACAGATTTATTTATTTT 1980  
QY 61 ATTTATTTT 73  
DB 1981 ATTTATTTT 1993  
RESULT 10  
196207 196207 3565 bp DNA linear PAT 01-DEC-1998  
LOCUS 196207  
DEFINITION Sequence 44 from patent US 5734039.  
ACCESSION 196207  
VERSION 196207.1 GI:3940677  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3565)  
AUTHORS Calabretta, B. and Skorski, T.  
TITLE Antisense oligonucleotides targeting cooperating oncogenes  
JOURNAL Patent: US 5734039-A 44 31-MAR-1998;  
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source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AACGTTTATGCTGTTTAAATTTATTTAATGATGATTCACAGATTTATTTATTTT 60  
DB 3353 AACGTTTATGCTGTTTAAATTTATTTAATGATGATTCACAGATTTATTTATTTT 3412  
QY 61 ATTTATTTT 73  
DB 3413 ATTTATTTT 3425  
RESULT 11  
AX330284 3565 bp DNA linear PAT 09-JAN-2002  
LOCUS AX330284  
DEFINITION Sequence 793 from Patent WO0194629.  
ACCESSION AX330284  
VERSION AX330284.1 GI:18103262  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 3565)  
AUTHORS Mamula, J.; Butera, J.; Primates; Catarrhini; Homidae; Homo.  
TITLE 1 (bases 1 to 3565)  
JOURNAL Fodor, G., Han, M., and Wiemann, S.  
COMMENT Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amd, C., Osanger, A.,  
The German Human CDNA Consortium  
Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuberger, GERMANY  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by AGOWA (Berlin/Germany) within the CDNA sequencing  
consortium of the German Genome Project.  
This clone (DKFZp686J04124) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further

```

ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS      Oellers,N., Gehrman,M., Kallabis,H., Hall,R., Schulze,T. and
              Kregel,C.
TITLE        Genes and proteins for prevention, prediction, diagnosis, prognosis
              and treatment of chronic lung disease
JOURNAL      Patent: WO 02097127-A 13 05-DEC-2002;
MEDLINE      Bayer Aktiengesellschaft (DE)
PUBMED       Location/Qualifiers
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Db      3353 AACGTTTATGCTTTTAAATTATTTATTAAGATGATTCAGATATTATATTTT 3412
              |||||
OY      61 ATTTTATTTT 73
Db      3413 ATTTTATTTT 3425
              |||||

RESULT 14
HSCFOS      HSCFOS      3565 bp      DNA      linear      PRI 21-NOV-1994
LOCUS       Human cellular oncogene c-fos (complete sequence).
DEFINITION V01512
ACCESSION   V01512
VERSION     V01512.1 GI:29903
KEYWORDS    oncogene.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 3565)
AUTHORS     Van Straaten,F., Muller,R., Curran,T., Van Beveren,C. and
              Verma,I.M.
TITLE       Complete nucleotide sequence of a human c-onc gene: deduced amino
              acid sequence of the human c-fos protein
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 80 (11), 3183-3187 (1983)
MEDLINE     83221560
PUBMED      6574479
COMMENT     Data kindly reviewed (10-OCT-1983) by F. van Straaten.
FEATURES
             Location/Qualifiers
             1. .3565
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
             132. .3515
                /gene="c-fos"
             132. .3515
                /gene="c-fos"
             132. .3515
                /note="possible transcript"
             132. .429,1183. .1434,1866. .1973,2088. .3515)
                /gene="c-fos"
             132. .3259
                /gene="c-fos"
             132. .429
                /note="possible transcript"
             132. .429,1183. .1434,1866. .1973,2088. .3239)
                /gene="c-fos"
             132. .429
                /note="(alternate start site)"
             136. .>3515
                /gene="c-fos"
             precursor_RNA
                /note="(alternate start site)"
             precursor_RNA
                /gene="c-fos"

```



Oy 61 ATTTATTTTTT 73  
| | | | | | | | | |  
Db 3965 ATTTATTTTTT 3977

Search completed: October 14, 2004, 18:09:30  
Job time : 2338 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 16:18:30 ; Search time 283 Seconds  
(without alignments)  
1095.825 Million cell updates/sec

Title: US-10-658-093-19

Perfect score: 73  
Sequence: 1 aacgtttatctgtgtttta.....cattttatttttttttt 73

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*

1: \_ geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	75	6	AAD46901 C-fos 3'
2	73	100.0	242	6	ABL37580 Human col
3	73	100.0	245	6	ABV94414 Breast ca
4	73	100.0	465	8	ACH22964 Human adu
5	73	100.0	477	9	ABZ35131 Human gen
6	73	100.0	477	9	ADBE84978 Farnesyl
7	73	100.0	1176	7	ABX62923 Human act
8	73	100.0	1918	9	ADD29870 Human tum
9	73	100.0	1946	4	AAI13509 Probe #34
10	73	100.0	1946	4	ABAS5207 Human foe
11	73	100.0	1946	4	AAI34869 Probe #35
12	73	100.0	1946	4	ABA44752 Human bre
13	73	100.0	1946	4	ABA24954 Probe #34
14	73	100.0	1946	4	AAK28922 Human bon
15	73	100.0	1946	4	AAK03468 Human bra
16	73	100.0	1946	5	AAI03394 Probe #33
17	73	100.0	1946	6	ABSO3451 Human gen
18	73	100.0	2084	6	ABV93327 Breast ca
19	73	100.0	2103	6	AAZ41352 Human nor
20	73	100.0	2165	8	ADB47308 Human CDN
21	73	100.0	2164	8	ACH04087 Human ova
22	73	100.0	2180	6	ABG54467 Human act
23	73	100.0	2227	7	ABX62920 Human act

24	73	100.0	2461	3	AAC98119 Human col
25	73	100.0	2461	4	AAH33223 Human col
26	73	100.0	3514	6	ABK50444 Human v-f
27	73	100.0	3565	3	AAV20466 Human c-f
28	73	100.0	3565	3	AAA34970 Human ade
29	73	100.0	3565	3	AAF21092 Human low
30	73	100.0	3565	6	AB168566 Kidney ca
31	73	100.0	3565	6	AB162456 Colon ade
32	73	100.0	3565	6	ABK84488 Human CDN
33	73	100.0	3565	6	ABK64754 Human ben
34	73	100.0	3565	7	ACC46762 Human COP
35	73	100.0	3565	7	ABZ96786 Human nuc
36	73	100.0	6210	2	AAO63815 c-fos gen
37	73	100.0	6210	3	AAH34969 Human ade
38	73	100.0	6210	3	AAE21091 Human low
39	73	100.0	6210	6	ABT10875 Human bre
40	73	100.0	6210	6	ABZ35089 Human gen
41	73	100.0	6210	7	ACC46752 Human COP
42	73	100.0	6210	7	ABZ96785 Human nuc
43	73	100.0	16595	3	AAH34973 Human ade
44	73	100.0	16595	3	AAE21095 Human low
45	73	100.0	16595	7	ABZ96789 Human nuc

## ALIGNMENTS

RESULT 1  
ID AAD46901 standard; DNA, 75 BP.  
XX AAD46901;  
AC AAD46901;  
XX 27-JAN-2003 (first entry)  
DT  
XX C-fos 3' UTR ARE DNA #1.  
DE  
XX Gene expression; transcript stability; drug screening; AU-rich element;  
KW ARE; c-fos; ds.  
RV  
XX Mammalia.  
OS  
XX WO200272844-A1.  
FN  
XX 19-SEP-2002.  
PD  
XX 08-MAR-2002; 2002MCO-AUD00351.  
PF  
XX 09-MAR-2001; 2001US-0274770P.  
PR  
XX (GENE-) GENE STREAM PTY LTD.  
PA  
XX Daily J;  
PI  
XX WPI; 2002-759847/82.  
DR  
XX New expression vector useful for modulating gene expression, identifying  
PT and analyzing regulatory sequences, new targets and reagents for treating  
PT human diseases, comprises a transcribable polynucleotide encoding an RNA  
PT element.  
XX  
XX Claim 11; Page 59; 1033P; English.  
XX  
XX The present invention relates to novel expression vectors and/or reporter  
CC vectors providing kinetics of protein expression with improved temporal  
CC correlation to the promoter activity. The expression vectors comprise  
CC transcribable polynucleotides having sequences of nucleotides encoding  
CC RNA elements which modulates the stability of a transcript corresponding  
CC to the transcribable polynucleotide. The expression vectors are useful  
CC for modulating the stability of a transcript and determining expression  
CC of a polynucleotide of interest. They are useful for modulating gene  
CC expression, identifying and analyzing regulatory sequences, new targets  
CC and reagents for treating human diseases and for drug screening. The



CC Present sequence is c-fos 3' UTR ARE (AU-rich element) DNA. This sequence  
 CC is used in the exemplification of the invention

XX Sequence 75 BP; 20 A; 3 C; 7 G; 45 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 6; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-06;  
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTTAATGATGATTCACATATTTATTTT 60  
 DB 3 AACGTTTATGCTGTTTAAATTATTTAATGATGATTCACATATTTATTTT 62  
 QY 61 ATTTATTTT 73  
 DB 63 ATTTATTTT 75

# RESULT 2

ABL37580/c  
 ID ABL37580 standard; cDNA; 242 BP.

XX ABL37580;

XX 08-APR-2002 (first entry)

XX Human colon tumour antigen polynucleotide SEQ ID NO:1169.

XX Human; colon cancer; colon tumour antigen; cytostatic; vaccine;

XX colon tumour metastatic antigen; diagnosis; gene; ss.

XX Homo sapiens.

XX WO200196388-A2.

XX 20-DEC-2001.

XX 08-JUN-2001; 2001WO-US018557.

XX 09-JUN-2000; 2000US-0210899P.

XX 20-FEB-2001; 2001US-0270216P.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Harlocker SL, Secret H;

XX WPI; 2002-114514/15.

XX Novel isolated colon tumor polynucleotide differentially expressed in  
 PT colon tumor or colon metastatic tumor and polypeptides encoded by them,  
 PT useful for inhibiting development of cancer in patient.

XX Claim 1; SEQ ID NO 1169; 105bp; English.

XX ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I)  
 CC which were isolated from human colon tumour and colon metastatic tumour  
 CC cDNA libraries. (I) have cytostatic activity and can be used in vaccine  
 CC production. (I) can be used for stimulating and/or expanding T cells  
 CC specific for a tumour protein on contact with the T cells. They are also  
 CC useful for inhibiting the development of cancer in a patient. (I) can be  
 CC used as probes or primers for nucleic acid hybridisation, for preparing  
 CC mutant species primers, or primers for use in genetic constructions. (I)  
 CC can be used in the diagnosis of a colon tumour

XX Sequence 242 BP; 102 A; 38 C; 21 G; 78 T; 0 U; 3 Other;

Query Match 100.0%; Score 73; DB 6; Length 242;

Best Local Similarity 100.0%; Pred. No. 6.2e-06;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTTAATGATGATTCACATATTTATTTT 60  
 DB 190 AACGTTTATGCTGTTTAAATTATTTAATGATGATTCACATATTTATTTT 131

QY 61 ATTTATTTT 73

DB 130 ATTTATTTT 118

# RESULT 3

ABV94414/c  
 ID ABV94414 standard; cDNA; 245 BP.

XX ABV94414;

XX 08-JAN-2003 (first entry)

XX Breast carcinoma related nucleotide sequence SEQ ID NO:405.

XX Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;  
 XX ss.

XX Homo sapiens.

XX WO200246467-A2.

XX 13-JUN-2002.

XX 07-DEC-2001; 2001WO-IB002811.

XX 08-DEC-2000; 2000US-0254090P.

XX 07-DEC-2001; 2001US-00007926.

XX (IPSO-) IPSOGEN.

XX Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Felt V;

XX WPI; 2002-619023/66.

XX Novel polynucleotide library useful in molecular characterization of a  
 PT carcinoma, comprising a pool of polynucleotide sequences or its  
 PT subsequences which are either underexpressed or overexpressed in tumor  
 PT cells.

XX Claim 1; Page 364; 401bp; English.

XX The present invention describes a polynucleotide library (I) useful in  
 CC the molecular characterization of a carcinoma, comprising a pool of  
 CC polynucleotides or its subsequences which are either underexpressed or  
 CC overexpressed in tumour cells, and correspond to any of the  
 CC polynucleotide sequences chosen from the 468 sequences given in ABV94010  
 CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for  
 CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting  
 CC (MI) differentially expressed polynucleotide sequences which are  
 CC correlated with a cancer, involves obtaining a polynucleotide sample from  
 CC a patient, and reacting the polynucleotide sample obtained with a probe  
 CC immobilised on a solid support, where the probe comprises any combination  
 CC of the polynucleotide sequences of (I) or its expression products encoded  
 CC by polynucleotide sequences of (I), and detecting the reaction product.  
 CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)  
 CC is useful in molecular characterization of a carcinoma. (I) and (II) are  
 CC useful for the prognosis or diagnostic of tumour, in differentiating a  
 CC normal cell from a cancer cell, detecting a hormone sensitive tumour  
 CC cell, differentiating a tumour with lymph nodes from a tumour without  
 CC lymph nodes, differentiating antineoplastic sensitive tumours from  
 CC antineoplastic-insensitive tumours, and classifying good and poor prognosis  
 CC primary breast tumours. (I) is useful for large-scale molecular  
 CC characterisation of breast cancer that help in prediction, prognosis and  
 CC cancer treatment, and for detecting differentially expressed genes that  
 CC correlated with a cancer

XX Sequence 245 BP; 101 A; 40 C; 25 G; 72 T; 0 U; 7 Other;

Query Match 100.0%; Score 73; DB 6; Length 245;

Best Local Similarity 100.0%; Pred. No. 6.2e-06;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATCTCAGATATTATATTTT 60
DB 180 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATCTCAGATATTATATTTT 121
QY 61 ATTTTATTTT 73
DB 120 ATTTTATTTT 108

RESULT 4
ACH22964
ID ACH22964 standard; cDNA; 465 BP.
XX
AC ACH22964;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human adult ovary cDNA #1344.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX
XX Claim 1; SEQ ID NO 10176; 44bp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?docID=20030073623
XX
XX Sequence 465 BP; 146 A; 58 C; 74 G; 169 T; 0 U; 18 Other;
XX
Query Match 100.0%; Score 73; DB 8; Length 465;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATCTCAGATATTATATTTT 60
DB 207 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATCTCAGATATTATATTTT 266
QY 61 ATTTTATTTT 73
DB 267 ATTTTATTTT 279

RESULT 5
ABZ35131/c
ID ABZ35131 standard; cDNA; 477 BP.
XX
AC ABZ35131;
XX
DT 05-FEB-2003 (first entry)
XX
DE Human gene expression profile polynucleotide SEQ ID NO 243.
XX
XX
KW Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW gene expression; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200274979-A2.
XX
PD 26-SEP-2002.
XX
PF 20-MAR-2002; 2002WO-US008456.
XX
PR 20-MAR-2001; 2001US-0276947P.
XX
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Wan J, Wang Y;
XX
WPI; 2002-740862/80.
XX
XX
XX New gene expression profile generated from primary, endothelial,
XX epithelial, and muscle cell types, useful for identifying disease
XX pathologies involving alterations of gene expression, e.g. cancer.
XX
XX
XX Claim 7; Page 427; 850bp; English.
XX
XX The invention relates to a gene expression profile comprising one or more
XX genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
XX is a coronary artery endothelium, umbilical artery or vein endothelium,
XX aortic endothelium, dermal microvascular endothelium, pulmonary artery
XX endothelium, myometrium microvascular endothelium, keratinocyte
XX epithelium, bronchial epithelium, mammary epithelium, prostate
XX epithelium, renal cortical epithelium, renal proximal tubule epithelium,
XX small airway epithelium, renal epithelium, umbilical artery smooth
XX muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
XX dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
XX aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
XX bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
XX osteoblasts or prostate stromal cell. The gene expression profile is used
XX for determining the level of RNA expression for a sample, determining the
XX phenotype of a cell and distinguishing cell types. The gene or a protein
XX expression profile is useful in identifying disease pathologies involving
XX alterations of gene expression. The assessment of expression profiles may
XX provide meaningful information with respect to tumour type and stage
XX treatment methods, and prognosis. The gene or protein expression profile
XX may also be used for creating microarrays. The microarray is useful for
XX genetic and physical mapping of genomes, DNA sequencing, genetic or
XX medical diagnosis, genotyping of organisms, confirming cell or tissue
XX identifications and in identifying promising antibiotics, antiviral or
XX antifungal agents
XX
XX Sequence 477 BP; 188 A; 85 C; 59 G; 144 T; 0 U; 1 Other;
```





XX MO200157277-A2.  
 PN  
 XX  
 PD 09-AUG-2001.  
 PF 30-JAN-2001; 2001WO-US000669.  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00633366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI; 2001-483447/52.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human fetal liver.  
 XX  
 PS Claim 1, SEQ ID NO 3512; 639pp + Sequence Listing; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe for measuring  
 CC human gene expression in a sample derived from human fetal liver. The  
 CC single exon nucleic acid probes may be used for predicting, measuring and  
 CC displaying gene expression in samples derived from human fetal liver. The  
 CC present sequence is a single exon nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 73; DB 4; Length 1946;  
 Best Local Similarity 100.0%; Pred. No. 5e-06; Mismatches 0; Gaps 0;  
 Matches 73; Conservative 0; Indels 0; Gaps 0;  
 QY 1 AACGTTTATGTTGTTTAAATTATTTAATTAAGATGATTCACAGATTTATATTTT 60  
 DB 1579 AACGTTTATGTTGTTTAAATTATTTAATTAAGATGATTCACAGATTTATATTTT 1638  
 QY 61 ATTTATTTTTTT 73  
 DB 1639 ATTTATTTTTTT 1651  
 XX  
 RESULT 11  
 AA134869  
 ID AA134869 standard; DNA; 1946 BP.  
 XX  
 AC AA134869;  
 XX  
 DT 17-OCT-2001 (first entry)  
 XX  
 DE Probe #355 used to measure gene expression in human placenta sample.  
 XX  
 KW Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PF 30-JAN-2001; 2001WO-US000663.  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI; 2001-488897/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human placenta.  
 XX  
 PS Claim 25, SEQ ID NO 3555; 654pp; English.  
 XX  
 CC The present invention relates to single exon nucleic acid probes (SENP).  
 CC The present sequence is one such probe. The probes are useful for  
 CC producing a microarray for predicting, measuring and displaying gene  
 CC expression in samples derived from human placenta. The probes are useful  
 CC for antenatal diagnosis of human genetic disorders  
 XX  
 SQ Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 73; DB 4; Length 1946;  
 Best Local Similarity 100.0%; Pred. No. 5e-06; Mismatches 0; Gaps 0;  
 Matches 73; Conservative 0; Indels 0; Gaps 0;  
 QY 1 AACGTTTATGTTGTTTAAATTATTTAATTAAGATGATTCACAGATTTATATTTT 60  
 DB 1579 AACGTTTATGTTGTTTAAATTATTTAATTAAGATGATTCACAGATTTATATTTT 1638  
 QY 61 ATTTATTTTTTT 73  
 DB 1639 ATTTATTTTTTT 1651  
 XX  
 RESULT 12  
 ABA44752  
 ID ABA44752 standard; DNA; 1946 BP.  
 XX  
 AC ABA44752;  
 XX  
 DT 01-FEB-2002 (first entry)  
 XX  
 DE Human breast cell single exon nucleic acid probe #3447.  
 XX  
 KW Human; microarray; single exon probe; gene expression; breast; disease;  
 KW cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PF 30-JAN-2001; 2001WO-US000662.  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI; 2001-496933/54.

PT New spatially-addressable set of single exon nucleic acid probes, useful  
 PT for measuring gene expression in sample derived from human breast,  
 PT comprises number of single exon nucleic acid probes.

XX Claim 1, SEQ ID NO 3447, 327bp + Sequence Listing; English.

XX The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human breast and BT 474 cells. The method involves contacting the  
 CC probes with a collection of detectably labelled nucleic acids derived  
 CC from mRNA of human breast, and then measuring the label bound to each  
 CC probe of the microarray. The probes are useful for verifying the  
 CC expression of regions of genomic DNA predicted to encode proteins. They  
 CC are useful for gene discovery, and for determining predisposition and/or  
 CC prognosing breast disease. Gene expression analysis is useful for  
 CC assessing the toxicity of chemical agents on cells. The microarray of  
 CC this invention presents a far greater diversity of probes for measuring  
 CC gene expression, with far less bias than expressed sequence tag  
 CC microarrays. The method is suitable for rapid production of functional  
 CC information from genomic sequence. The present sequence is a single exon  
 CC nucleic acid probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1946 BP, 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 4; Length 1946;

Best Local Similarity 100.0%; Pred. No. 5e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATTGCTGTTTAAATTATTTAAGATGATTCGAGATTTATTAATTTT 60  
 DB 1579 AACGTTTATTGCTGTTTAAATTATTTAAGATGATTCGAGATTTATTAATTTT 1638

QY 61 ATTTATTTT 73  
 DB 1639 ATTTATTTT 1651

#### RESULT 13

ABA24954  
 ID ABA24954 standard; DNA, 1946 BP.

XX ABA24954;

DT 23-JAN-2002 (first entry)

DE Probe #3420 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease; ss.

OS Homo sapiens.

XX MO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLB-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX MPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human  
 PT hearts.

XX Claim 1, SEQ ID NO 3420; 530bp; English.

XX The present invention relates to single exon nucleic acid probes for  
 CC measuring human gene expression in a sample derived from human heart. The  
 CC present sequence is one such probe. The probes may be used for  
 CC predicting, measuring and displaying gene expression in samples derived  
 CC from the human heart via microarrays. By measuring gene expression, the  
 CC probes are useful for predicting, diagnosing, grading, staging,  
 CC monitoring and prognosing diseases of the human heart and vascular system  
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
 CC congenital heart disease. Note: The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1946 BP, 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 4; Length 1946;

Best Local Similarity 100.0%; Pred. No. 5e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATTGCTGTTTAAATTATTTAAGATGATTCGAGATTTATTAATTTT 60  
 DB 1579 AACGTTTATTGCTGTTTAAATTATTTAAGATGATTCGAGATTTATTAATTTT 1638

QY 61 ATTTATTTT 73  
 DB 1639 ATTTATTTT 1651

#### RESULT 14

AAK28922  
 ID AAK28922 standard; DNA, 1946 BP.

XX AAK28922;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed single exon probe SEQ ID NO: 3479.

XX Human; bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.

OS Homo sapiens.

XX MO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLB-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX MPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human bone marrow.

PS Example 4; SEQ ID NO 3479; 658bp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukemia and myeloma. The present sequence is one of  
 CC the probes of the invention  
 XX  
 SQ Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 73; DB 4; Length 1946;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGTTTATGCTGTTTAAATTATTTAATTAAGATGATTCGATGATTTATATTTT 60  
 DB 1579 AACGTTTATGCTGTTTAAATTATTTAATTAAGATGATTCGATGATTTATATTTT 1638  
 QY 61 ATTTATTTTTTT 73  
 DB 1639 ATTTATTTTTTT 1651  
 RESULT 15  
 AAK03468  
 ID AAK03468 standard; DNA; 1946 BP.  
 AC AAK03468;  
 XX  
 XX AAK03468;  
 AC  
 XX  
 DT 05-NOV-2001 (first entry)  
 XX  
 DE Human brain expressed single exon probe SEQ ID NO: 3459.  
 XX  
 KW Human; brain expressed exon; gene expression analysis; probe; microarray;  
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 OS  
 XX  
 FN WO200157275-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PE 30-JAN-2001; 2001WO-US000667.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-483446/52.  
 XX  
 FT Single exon nucleic acid probes for analyzing gene expression in human  
 FT brains.  
 PT  
 PS Example 4; SEQ ID NO 3459; 650bp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is one of the probes of the  
 CC invention  
 XX

SQ Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 73; DB 4; Length 1946;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGTTTATGCTGTTTAAATTATTTAATTAAGATGATTCGATGATTTATATTTT 60  
 DB 1579 AACGTTTATGCTGTTTAAATTATTTAATTAAGATGATTCGATGATTTATATTTT 1638  
 QY 61 ATTTATTTTTTT 73  
 DB 1639 ATTTATTTTTTT 1651  
 Search completed: October 14, 2004, 17:30:27  
 Job time : 288 secs

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 17:26:59 ; Search time 59 Seconds

(without alignments)  
686.634 Million cell updates/sec

Title: US-10-658-093-19

Perfect score: 73  
Sequence: 1 aacgttttttctgttttta.....tattttattttttttt 73Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents NA:\*

- 1: /cgnt2\_6/prodata/2/ina/5A\_COMB.seq:\*
- 2: /cgnt2\_6/prodata/2/ina/5B\_COMB.seq:\*
- 3: /cgnt2\_6/prodata/2/ina/6A\_COMB.seq:\*
- 4: /cgnt2\_6/prodata/2/ina/6B\_COMB.seq:\*
- 5: /cgnt2\_6/prodata/2/ina/PCTUS\_COMB.seq:\*
- 6: /cgnt2\_6/prodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	100.0	3565	1 US-08-306-691B-44	Sequence 44, Appl
2	73	100.0	3565	5 PCT-US93-06251-20	Sequence 20, Appl
3	71.4	97.8	402	4 US-09-702-705-571	Sequence 571, Appl
4	71.4	97.8	402	4 US-09-702-705-579	Sequence 579, Appl
5	71.4	97.8	402	4 US-09-736-457-571	Sequence 571, Appl
6	71.4	97.8	402	4 US-09-736-457-579	Sequence 579, Appl
7	71.4	97.8	402	4 US-09-614-124B-571	Sequence 571, Appl
8	71.4	97.8	402	4 US-09-614-124B-579	Sequence 579, Appl
9	71.4	97.8	402	4 US-09-671-325-571	Sequence 571, Appl
10	71.4	97.8	402	4 US-09-671-325-579	Sequence 579, Appl
11	71.4	97.8	402	4 US-09-589-184-571	Sequence 571, Appl
12	71.4	97.8	402	4 US-09-589-184-579	Sequence 579, Appl
13	69	94.5	69	1 US-08-146-421-2	Sequence 2, Appl
14	40	54.8	68	4 US-09-320-609-3	Sequence 3, Appl
15	37.8	51.8	6040	4 US-10-204-708-70	Sequence 70, Appl
16	36.2	49.6	5476	4 US-10-204-708-82	Sequence 82, Appl
17	35.8	49.0	196	4 US-09-644-460-40	Sequence 40, Appl
18	35.4	48.5	2621	2 US-08-553-619B-8	Sequence 8, Appl
19	35.4	48.5	5455	4 US-10-204-708-34	Sequence 34, Appl
20	35.4	48.5	9347	4 US-10-204-708-35	Sequence 35, Appl
21	34.8	47.7	1664976	4 US-08-916-421B-1	Sequence 1, Appl
22	34.6	47.4	10467	4 US-10-204-708-2	Sequence 2, Appl
23	34.6	47.4	10482	4 US-09-322-478-23	Sequence 23, Appl
24	34.4	47.1	1190	4 US-09-390-207-1	Sequence 1, Appl
25	34.4	47.1	5562	4 US-10-204-708-63	Sequence 63, Appl
26	34.4	47.1	6040	4 US-10-204-708-69	Sequence 69, Appl
27	34.4	47.1	6243	2 US-09-056-075-1	Sequence 1, Appl

28	34.4	47.1	8607	4 US-10-204-708-71	Sequence 71, Appl
29	34.4	47.1	10457	4 US-10-204-708-1	Sequence 1, Appl
30	34.4	47.1	51719	4 US-09-918-686-2	Sequence 2, Appl
31	34.4	47.1	92139	4 US-09-918-686-1	Sequence 1, Appl
32	34.2	46.8	351	4 US-09-621-976-16138	Sequence 16138, A
33	34.2	46.8	62804	4 US-09-800-960-3	Sequence 3, Appl
34	34.2	46.8	62804	4 US-10-096-960-3	Sequence 3, Appl
35	34	46.6	2683	1 US-08-136-743B-3	Sequence 3, Appl
36	33.8	46.3	787	4 US-09-621-976-1878	Sequence 1878, Ap
37	33.8	46.3	1683	3 US-09-347-803-11	Sequence 11, Appl
38	33.8	46.3	6306	4 US-10-204-708-50	Sequence 50, Appl
39	33.8	46.3	6801	4 US-10-204-708-62	Sequence 62, Appl
40	33.8	46.3	11049	4 US-10-204-708-24	Sequence 24, Appl
41	33.6	46.0	8861	4 US-10-204-708-80	Sequence 80, Appl
42	33.6	46.0	19124	2 US-08-487-826B-13	Sequence 13, Appl
43	33.4	45.8	212	4 US-09-621-976-1325	Sequence 1325, Ap
44	33.4	45.8	268	4 US-09-621-976-73	Sequence 73, Appl
45	33.4	45.8	970	4 US-09-833-381-1294	Sequence 1294, Ap

## ALIGNMENTS

RESULT 1  
US-08-306-691B-44  
Sequence 44, Application US/08306691B  
Patent No. 5734039  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
TITLE OF INVENTION: ANTISENSE  
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESS: Seidel, Gonda, Lavorgna & Monaco, P.C.  
STREET: Two Penn Center, Suite 1800  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3565 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-306-691B-44  
Query Match 100.0%; Score 73; DB 1; Length 3565;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 AACGTTTATGCTGTTTAAATTATTTATTAAGATGATTCCTCAGAAATTATATTTT 60



Db 3353 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 3412

QY 61 ATTTATTTTTT 73

Db 3413 ATTTATTTTTT 3425

RESULT 2  
PCT-US93-06251-20

; Sequence 20, Application PC/RUS9306251

; GENERAL INFORMATION:

; APPLICANT: Wickstrom, Eric and Rife, Jason P.

; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing

; NUMBER OF SEQUENCES: 93

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: NY

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/06251

; FILING DATE: 19930630

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Digilio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 8586

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 516-742-4343

; TELEFAX: 516-742-4366

; TELEX: 230 901 SAMS UR

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3565 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULAR TYPE: DNA (genomic)

; PCT-US93-06251-20

Query Match 100.0%; Score 73; DB 5; Length 3565;

Best Local Similarity 100.0%; Pred. No. 1.4e-08;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 60

Db 3353 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 3412

QY 61 ATTTATTTTTT 73

Db 3413 ATTTATTTTTT 3425

RESULT 3  
US-09-702-705-571

; Sequence 571, Application US/09702705

; Patent No. 6504010

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705

; CURRENT FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 1833

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 571

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Homo sapien

; US-09-702-705-571

Query Match 97.8%; Score 71.4; DB 4; Length 402;

Best Local Similarity 98.6%; Pred. No. 3.4e-08;

Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 60

Db 225 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 284

QY 61 ATTTATTTTTT 73

Db 285 ATTTATTTGTT 297

RESULT 4  
US-09-702-705-579

; Sequence 579, Application US/09702705

; Patent No. 6504010

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705

; CURRENT FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 1833

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 579

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Homo sapien

; US-09-702-705-579

Query Match 97.8%; Score 71.4; DB 4; Length 402;

Best Local Similarity 98.6%; Pred. No. 3.4e-08;

Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 60

Db 225 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 284

QY 61 ATTTATTTTTT 73

Db 285 ATTTATTTGTT 297

RESULT 5  
US-09-736-457-571

; Sequence 571, Application US/09736457

; Patent No. 6509448

```

; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaifanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-571

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Query Match          97.8%; Score 71.4; DB 4; Length 402;
Best Local Similarity 98.6%; Pred. No. 3.4e-08;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AACGTTTATGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTT 60
Db 225 AACGTTTATGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTT 284

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```

QY 61 ATTTATTTT 73
Db 285 ATTTATTTGTTT 297

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RESULT 6
US-09-736-457-579
; Sequence 579, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaifanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 579
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-579

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Query Match          97.8%; Score 71.4; DB 4; Length 402;
Best Local Similarity 98.6%; Pred. No. 3.4e-08;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AACGTTTATGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTT 60
Db 225 AACGTTTATGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTT 284

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QY 61 ATTTATTTT 73
Db 285 ATTTATTTGTTT 297

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RESULT 7
US-09-614-124B-571
; Sequence 571, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaifanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-571

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Query Match          97.8%; Score 71.4; DB 4; Length 402;
Best Local Similarity 98.6%; Pred. No. 3.4e-08;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AACGTTTATGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTT 60
Db 225 AACGTTTATGCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTT 284

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```

QY 61 ATTTATTTT 73
Db 285 ATTTATTTGTTT 297

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RESULT 8
US-09-614-124B-579
; Sequence 579, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaifanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 579
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-579

```

```

Query Match          97.8%; Score 71.4; DB 4; Length 402;
Best Local Similarity 98.6%; Pred. No. 3.4e-08;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	1758	AAATTTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	1817							
Qy	61	ATTTATTTT	73							
Db	1818	TTTTTAAATTT	1830							

Search completed: October 14, 2004, 18:42:43  
 Job time : 69 secs

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 18:09:36 ; Search time 341 Seconds  
(without alignments)

1085.274 Million cell updates/sec

Title: US-10-658-093-19

Perfect score: 73  
Sequence: 1 aacgtttatctgctttta.....tattttatttttttt 73

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
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6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_PUB\_PUB.seq:\*  
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18: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	73	US-10-658-093-19	Sequence 19, App1
2	73	100.0	75	US-10-658-093-14	Sequence 14, App1
3	73	100.0	237	US-10-085-783A-34451	Sequence 34451, A
4	73	100.0	237	US-10-242-535A-34451	Sequence 34451, A
5	73	100.0	239	US-09-878-178-1169	Sequence 1169, Ap
6	73	100.0	239	US-10-046-935-1169	Sequence 1169, Ap
7	73	100.0	239	US-10-146-502-1169	Sequence 1169, Ap
8	73	100.0	240	US-10-085-783A-30739	Sequence 30739, A
9	73	100.0	240	US-10-242-535A-30739	Sequence 30739, A
10	73	100.0	245	US-10-007-926A-405	Sequence 405, App
11	73	100.0	255	US-10-085-783A-893	Sequence 893, App
12	73	100.0	255	US-10-242-535A-893	Sequence 893, App
13	73	100.0	265	US-10-085-783A-19213	Sequence 19213, A
14	73	100.0	265	US-10-242-535A-19213	Sequence 19213, A

15	73	100.0	281	13	US-10-085-783A-26860	Sequence 26860, A
16	73	100.0	281	16	US-10-242-535A-26860	Sequence 26860, A
17	73	100.0	360	13	US-10-085-783A-29586	Sequence 29586, A
18	73	100.0	360	16	US-10-242-535A-29586	Sequence 29586, A
19	73	100.0	465	10	US-09-918-995-10176	Sequence 10176, A
20	73	100.0	477	15	US-10-101-510-243	Sequence 129, App
21	73	100.0	477	17	US-10-283-975A-197	Sequence 197, App
22	73	100.0	1176	14	US-10-002-600-39	Sequence 39, App1
23	73	100.0	1613	16	US-10-062-674-2057	Sequence 2057, Ap
24	73	100.0	1946	9	US-09-864-761-3420	Sequence 3420, Ap
25	73	100.0	2084	15	US-10-007-926A-318	Sequence 318, App
26	73	100.0	2084	16	US-10-341-434-173	Sequence 173, App
27	73	100.0	2135	10	US-09-971-392-8	Sequence 8, App1
28	73	100.0	2154	13	US-10-116-802-292	Sequence 292, App
29	73	100.0	2180	16	US-10-264-049-347	Sequence 347, App
30	73	100.0	2227	14	US-10-002-600-36	Sequence 36, App1
31	73	100.0	2461	9	US-09-925-299-129	Sequence 129, App
32	73	100.0	2461	10	US-09-925-299-129	Sequence 129, App
33	73	100.0	2461	15	US-10-106-698-289	Sequence 289, App
34	73	100.0	3565	10	US-09-960-706-993	Sequence 993, App
35	73	100.0	3565	10	US-09-873-319-649	Sequence 649, App
36	73	100.0	3565	12	US-09-873-367C-793	Sequence 793, App
37	73	100.0	3565	12	US-09-968-007A-433	Sequence 433, App
38	73	100.0	6210	13	US-10-240-425-1272	Sequence 1272, Ap
39	73	100.0	6210	15	US-10-101-510-201	Sequence 201, App
40	73	100.0	6210	16	US-10-440-464-135	Sequence 135, App
41	73	100.0	6210	17	US-10-717-597-141	Sequence 141, App
42	73	100.0	6210	17	US-10-775-169-188	Sequence 188, App
43	73	100.0	22477	13	US-10-087-192-1554	Sequence 1594, Ap
44	71.4	97.8	402	9	US-09-736-457-571	Sequence 571, App
45	71.4	97.8	402	9	US-09-736-457-579	Sequence 579, App

#### ALIGNMENTS

RESULT 1  
US-10-658-093-19  
Sequence 19, Application US/10658093  
Publication No. US20040115704A1  
GENERAL INFORMATION:  
APPLICANT: Daly, John Michael  
TITLE OF INVENTION: Constructs for Gene Expression Analysis  
FILE REFERENCE: 12177722  
CURRENT APPLICATION NUMBER: US/10/658, 093  
CURRENT FILING DATE: 2003-09-09  
PRIOR APPLICATION NUMBER: USN 60/274770  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: PCT/AU02/00351  
PRIOR FILING DATE: 2001-03-08  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 19  
LENGTH: 73  
TYPE: DNA  
ORGANISM: mammalian  
US-10-658-093-19

Query Match 100.0%; Score 73; DB 17; Length 73;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTAAATTATTTATAGATGATTCACATATTTATTTT 60  
DB 1 AACGTTTATGCTTTTAAATTATTTATAGATGATTCACATATTTATTTT 60  
QY 61 ATTATATTTT 73  
DB 61 ATTATATTTT 73

RESULT 2  
US-10-658-093-14

Sequence 14, Application US/10658093  
Publication No. US20040115704A1  
GENERAL INFORMATION:  
APPLICANT: Daly, John Michael  
TITLE OF INVENTION: Constructs for Gene Expression Analysis  
FILE REFERENCE: 12177722  
CURRENT APPLICATION NUMBER: US/10/658,093  
CURRENT FILING DATE: 2003-09-09  
PRIOR APPLICATION NUMBER: US/03-09  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: PCT/AU02/00351  
PRIOR FILING DATE: 2001-03-08  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 14  
LENGTH: 75  
TYPE: DNA  
ORGANISM: mammalian  
US-10-658-093-14

Query Match 100.0%; Score 73; DB 17; Length 75;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTATTTATTTAATTAAGATGATTCAGATATTATTTT 60  
DB 3 AACGTTTATGCTTTTATTTAATTTAATTAAGATGATTCAGATATTATTTT 62  
QY 61 ATTTATTTTTTT 73  
DB 63 ATTTATTTTTTT 75

RESULT 3  
US-10-085-783A-34451  
Sequence 34451, Application US/10085783A  
Publication No. US20040037841A1  
GENERAL INFORMATION:  
APPLICANT: ChondroGene Inc.  
APPLICANT: Liaw, C.C.  
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
FILE REFERENCE: 4231/2002  
CURRENT APPLICATION NUMBER: US/10/085,783A  
CURRENT FILING DATE: 2002-02-28  
PRIOR APPLICATION NUMBER: US 60/305,340  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: US 60/275,017  
PRIOR FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: US 60/271,955  
PRIOR FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 58994  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 34451  
LENGTH: 237  
TYPE: DNA  
ORGANISM: Human  
US-10-085-783A-34451

Query Match 100.0%; Score 73; DB 13; Length 237;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTATTTAATTTAATTAAGATGATTCAGATATTATTTT 60  
DB 62 AACGTTTATGCTTTTATTTAATTTAATTAAGATGATTCAGATATTATTTT 121  
QY 61 ATTTATTTTTTT 73  
DB 122 ATTTATTTTTTT 134

RESULT 4  
US-10-242-535A-34451

Sequence 34451, Application US/10242535A  
Publication No. US20040013663A1  
GENERAL INFORMATION:  
APPLICANT: ChondroGene Inc.  
APPLICANT: Liaw, C.C.  
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
FILE REFERENCE: 4231/2005  
CURRENT APPLICATION NUMBER: US/10/242,535A  
CURRENT FILING DATE: 2002-09-12  
PRIOR APPLICATION NUMBER: US 10/085,783  
PRIOR FILING DATE: 2002-02-28  
PRIOR APPLICATION NUMBER: US 60/305,340  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: US 60/275,017  
PRIOR FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: US 60/271,955  
PRIOR FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 58994  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 34451  
LENGTH: 237  
TYPE: DNA  
ORGANISM: Human  
US-10-242-535A-34451

Query Match 100.0%; Score 73; DB 16; Length 237;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTATTTAATTTAATTAAGATGATTCAGATATTATTTT 60  
DB 62 AACGTTTATGCTTTTATTTAATTTAATTAAGATGATTCAGATATTATTTT 121  
QY 61 ATTTATTTTTTT 73  
DB 122 ATTTATTTTTTT 134

RESULT 5  
US-09-878-178-1169/C  
Sequence 1169, Application US/09878178  
Patent No. US2002017552A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugu  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER  
FILE REFERENCE: 210121.527  
CURRENT APPLICATION NUMBER: US/09/878,178  
CURRENT FILING DATE: 2001-06-08  
NUMBER OF SEQ ID NOS: 2237  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1169  
LENGTH: 239  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: miec feature  
LOCATION: (1) -- (239)  
OTHER INFORMATION: n = A,T,C or G  
US-09-878-178-1169

Query Match 100.0%; Score 73; DB 9; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTATTTAATTTAATTAAGATGATTCAGATATTATTTT 60  
DB 190 AACGTTTATGCTTTTATTTAATTTAATTAAGATGATTCAGATATTATTTT 131  
QY 61 ATTTATTTTTTT 73

Db 130 ATTTATTTTTTT 118

## RESULT 6

US-10-046-935-1169/c  
 / Sequence 1169, Application US/10046935  
 / Publication No. US20020156011A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Jhang, Yuglu  
 / APPLICANT: Harlocker, Susan L.  
 / APPLICANT: Secrist, Heather  
 / APPLICANT: Wang, Aijun  
 / APPLICANT: Stolk, John A.  
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 / FILE REFERENCE: 210121.527C1  
 / CURRENT APPLICATION NUMBER: US/10/046,935  
 / CURRENT FILING DATE: 2002-01-15  
 / NUMBER OF SEQ ID NOS: 2239  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 1169  
 / LENGTH: 239  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 223  
 / OTHER INFORMATION: n = A,T,C or G  
 US-10-046-935-1169

Query Match 100.0%; Score 73; DB 14; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-06;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTAAATTATTTAATTAAGATGATTCAGATATTTATTTT 60

Db 190 AACGTTTATGCTTTTAAATTATTTAATTAAGATGATTCAGATATTTATTTT 131

QY 61 ATTTATTTTTTT 73

Db 130 ATTTATTTTTTT 118

## RESULT 7

US-10-146-502-1169/c  
 / Sequence 1169, Application US/10146502  
 / Publication No. US20030069180A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Jhang, Yuglu  
 / APPLICANT: Harlocker, Susan L.  
 / APPLICANT: Secrist, Heather  
 / APPLICANT: Wang, Aijun  
 / APPLICANT: Stolk, John A.  
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 / FILE REFERENCE: 210121.527C2  
 / CURRENT APPLICATION NUMBER: US/10/146,502  
 / CURRENT FILING DATE: 2002-05-14  
 / NUMBER OF SEQ ID NOS: 2241  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 1169  
 / LENGTH: 239  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 223  
 / OTHER INFORMATION: n = A,T,C or G  
 US-10-146-502-1169

Query Match 100.0%; Score 73; DB 15; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-06;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTAAATTATTTAATTAAGATGATTCAGATATTTATTTT 60

Db 190 AACGTTTATGCTTTTAAATTATTTAATTAAGATGATTCAGATATTTATTTT 131

QY 61 ATTTATTTTTTT 73

Db 130 ATTTATTTTTTT 118

## RESULT 8

US-10-085-783A-30739  
 / Sequence 30739, Application US/10085783A  
 / Publication No. US20040037841A1  
 / GENERAL INFORMATION:  
 / APPLICANT: ChondroGene Inc.  
 / APPLICANT: Liew, C.C.  
 / TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 / FILE REFERENCE: 4231/2002  
 / CURRENT APPLICATION NUMBER: US/10/085,783A  
 / CURRENT FILING DATE: 2002-02-28  
 / PRIOR APPLICATION NUMBER: US 60/305,340  
 / PRIOR FILING DATE: 2001-07-13  
 / PRIOR APPLICATION NUMBER: US 60/275,017  
 / PRIOR FILING DATE: 2001-03-12  
 / PRIOR APPLICATION NUMBER: US 60/271,955  
 / PRIOR FILING DATE: 2001-02-28  
 / NUMBER OF SEQ ID NOS: 58994  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO 30739  
 / LENGTH: 240  
 / TYPE: DNA  
 / ORGANISM: Human  
 US-10-085-783A-30739

Query Match 100.0%; Score 73; DB 13; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-06;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTAAATTATTTAATTAAGATGATTCAGATATTTATTTT 60

Db 62 AACGTTTATGCTTTTAAATTATTTAATTAAGATGATTCAGATATTTATTTT 121

QY 61 ATTTATTTTTTT 73

Db 122 ATTTATTTTTTT 134

## RESULT 9

US-10-242-535A-30739  
 / Sequence 30739, Application US/10242535A  
 / Publication No. US20040013663A1  
 / GENERAL INFORMATION:  
 / APPLICANT: ChondroGene Inc.  
 / APPLICANT: Liew, C.C.  
 / TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 / FILE REFERENCE: 4231/2005  
 / CURRENT APPLICATION NUMBER: US/10/242,535A  
 / CURRENT FILING DATE: 2002-09-12  
 / PRIOR APPLICATION NUMBER: US 10/085,783  
 / PRIOR FILING DATE: 2002-02-28  
 / PRIOR APPLICATION NUMBER: US 60/305,340  
 / PRIOR FILING DATE: 2001-07-13  
 / PRIOR APPLICATION NUMBER: US 60/275,017  
 / PRIOR FILING DATE: 2001-03-12  
 / PRIOR APPLICATION NUMBER: US 60/271,955  
 / PRIOR FILING DATE: 2001-02-28  
 / NUMBER OF SEQ ID NOS: 58994  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO 30739  
 / LENGTH: 240  
 / TYPE: DNA  
 / ORGANISM: Human



US-10-242-535A-30739

Query Match 100.0%; Score 73; DB 16; Length 240;

Best Local Similarity 100.0%; Pred. No. 1.4e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTTTAAAGATGATCTCAGATATTATTTT 60  
|||||  
DB 62 AACGTTTATGCTGTTTAAATTTTAAAGATGATCTCAGATATTATTTT 121  
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QY 61 ATTTTATTTT 73  
|||||  
DB 122 ATTTTATTTT 134  
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RESULT 10  
US-10-007-926A-405/c

Sequence 405, Application US/10007926A

Publication No. US20030143539A1

GENERAL INFORMATION:

APPLICANT: BERTUCCI, FRANCOIS

APPLICANT: HOUUGATTE, REMI

APPLICANT: BIRBAUD, DANIEL

APPLICANT: NGUYEN, CATHERINE

APPLICANT: VIENS, PATRICE

APPLICANT: FERT, VINCENT

TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

FILE REFERENCE: 1546-R-00

CURRENT APPLICATION NUMBER: US/10/007,926A

CURRENT FILING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: 60/254,090

PRIOR FILING DATE: 2000-12-08

NUMBER OF SEQ ID NOS: 468

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 405

LENGTH: 245

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: 5' terminal sequence. v-fos fdj murine

OTHER INFORMATION: osteosarcoma viral oncogene homolog (fos) gene.

FEATURE:

NAME/KEY: modified\_base

LOCATION: (204)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (223)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (230)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (234)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (237)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (240)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

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NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

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NAME/KEY: modified\_base

LOCATION: (242)

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NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

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NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

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LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:

NAME/KEY: modified\_base

LOCATION: (242)

OTHER INFORMATION: a, t, c or g

FEATURE:



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd

OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 17:17:37 ; Search time 1912 Seconds  
(without alignments)  
1140.136 Million cell updates/sec

Title: US-10-658-093-19  
Perfect score: 73  
Sequence: 1 aacgtctcatgtgcttta.....tattctattctatctctt 73

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

```
Searched:      27513289 segs, 14931090276 residues
Total number of hits satisfying chosen parameters:  55026578
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
```

## SUMMARIES

Result	Query	Score	Match	length	ID	Description
C 1	73	100.0	183	10	BE827983	RC4-ET002
C 2	73	100.0	214	14	CA842273	1Q39412..*
C 3	73	100.0	216	14	D58202	D58202 HUM3550D5B
C 4	73	100.0	233	14	R79209	R79209 Y188B05..B1

C 5	73	100.0	245	9	AA020879	AE64G03.r
C 6	73	100.0	284	14	D57391	AA020879
C 7	73	100.0	291	12	BM955729	BM955729
C 8	73	100.0	331	10	BF436555	BF436555
C 9	73	100.0	334	10	BF752720	RC4-BN040
C 10	73	100.0	337	10	CA5147336	AA744736
C 11	73	100.0	338	14	CA771107	io70h05.x
C 12	73	100.0	339	14	CA434443	CA434443
C 13	73	100.0	350	14	CB068539	CB068539
C 14	73	100.0	351	9	AM021706	AM021706
C 15	73	100.0	352	14	CB068661	1s31d11.x
C 16	73	100.0	353	13	BU727713	UI-B-CR0-
C 17	73	100.0	354	10	AM118330	x67b02.x
C 18	73	100.0	354	12	BM993176	UI-H-DT0-
C 19	73	100.0	355	14	CA448668	UI-H-EI0-
C 20	73	100.0	357	12	BM509895	BM509895
C 21	73	100.0	358	10	BF711757	MI-P-A2-a
C 22	73	100.0	360	12	BM658610	TOH602768
C 23	73	100.0	367	14	N68137	Y25G10.b1
C 24	73	100.0	368	10	BF654301	BF654301
C 25	73	100.0	378	9	AA631437	NP85C10.b
C 26	73	100.0	378	10	BF773649	BF773649
C 27	73	100.0	379	14	N23726	Yw46G07.a1
C 28	73	100.0	393	9	AM021936	df30F04.y
C 29	73	100.0	393	14	N66497	Yz44D03.b1
C 30	73	100.0	411	13	BX091171	BM091171
C 31	73	100.0	412	10	BE754739	208340.MA
C 32	73	100.0	416	10	BE813852	BE813852
C 33	73	100.0	416	12	BQ029194	QV3-BN004
C 34	73	100.0	420	14	CB466312	UI-H-DT0-
C 35	73	100.0	420	14	CB857918	NISC.na10
C 36	73	100.0	421	10	BE754742	NISC.na10
C 37	73	100.0	422	9	AV591653	BE754742
C 38	73	100.0	422	12	BG301114	AV591653
C 39	73	100.0	423	10	BE041558	HOA53-I-H
C 40	73	100.0	424	9	AI348684	ho3e11.x
C 41	73	100.0	425	12	BM504570	q025G07.x
C 42	73	100.0	428	12	BM5051320	1987G10.x
C 43	73	100.0	439	9	AUI185330	1975h06.x
C 44	73	100.0	435	9	AA022208	AUI185330
C 45	73	100.0	436	9	AA985597	AA022208
						df34d03.y
						AA985597
						cg84a10.s

## ALIGNMENTS

	RESULT 1				
BE827983/c	183 bp	mrna	linear	EST 22-SEP-2000	
LOCUS	BE827983				
DEFINITION	RC4-ET0024-290500-013-e10 ET0024	Homo sapiens	cDNA,	mrna	sequence.
ACCESSION	BE827983				
VERSION	BE827983.1	GI:10260361			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (Dasea 1 to 183)				
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,				

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
PIRNUM	10737800
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Rudwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,



QY 1 AACGTTTATGCTGTTTATTTATTTATTTAGATGATCGACATATTTATTTT 60  
 |||  
 DB 35 AACGTTTATGCTGTTTATTTATTTATTTAGATGATCGACATATTTATTTT 94  
 |||  
 QY 61 ATTTATTTT 73  
 |||  
 DB 95 ATTTATTTT 107  
 |||

RESULT 4  
 R79209/c  
 LOCUS  
 DEFINITION R79209 243 bp mRNA linear EST 09-JUN-1995  
 Y188b05.a1 Soares placenta Nb2HP Homo sapiens cDNA clone  
 IMAGE:146289 3' similar to gb:V01512\_rnas P55-C-FOS PROTO-ONCOGENE  
 PROTEIN (HUMAN); mRNA sequence.

ACCESSION  
 VERSION R79209  
 KEYWORDS EST.  
 SOURCE R79209.1 GI:855490  
 ORGANISM Homo sapiens (human)

REFERENCE  
 AUTHORS Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 243)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Natta, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M.B., Tan, F.,  
 Trevaaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and  
 Wilson, R.

TITLE The Mashu-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

Insert Size: 800  
 High quality sequence stops: 241  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 800 Std Error: 0.00  
 Seq primer: Promega -21m13  
 High quality sequence stop: 241.  
 Location/Qualifiers

FEATURES  
 source  
 1..243  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:557815"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:146289"  
 /sex="female"  
 /dev\_stage="placenta obtained at birth (full term)"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares placenta Nb2HP"  
 /note="Organ: placenta; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 AACGGAAGATTCGCGCGCGACGAGATTTTATTTTATTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaudo. "

ORIGIN  
 Query Match 100.0%; Score 73; DB 14; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 0.0059;  
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTATTTATTTATTTAGATGATCGACATATTTATTTT 60  
 |||  
 DB 155 AACGTTTATGCTGTTTATTTATTTATTTAGATGATCGACATATTTATTTT 96  
 |||

QY 61 ATTTATTTT 73  
 |||  
 DB 95 ATTTATTTT 83  
 |||

RESULT 5  
 AA020879/c  
 LOCUS  
 DEFINITION AA020879 245 bp mRNA linear EST 30-JAN-1997  
 z64903.r1 Soares retina Nb24HR Homo sapiens cDNA clone  
 IMAGE:363796 5' similar to gb:V01512\_rnas P55-C-FOS PROTO-ONCOGENE  
 PROTEIN (HUMAN); mRNA sequence.

ACCESSION  
 VERSION AA020879  
 KEYWORDS EST.  
 SOURCE AA020879.1 GI:1484650  
 ORGANISM Homo sapiens (human)

REFERENCE  
 AUTHORS Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 245)  
 Hillier, L., Lennon, G., Becker, M., Bonaudo, M.F., Chiapelli, B.,  
 Chispe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,  
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,  
 Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,  
 Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
 Trevaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.  
 and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags  
 JOURNAL Genome Res. 6 (9), 807-828 (1996)  
 MEDLINE 97044478  
 PUBMED 8889549

COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

Insert Size: 800  
 High quality sequence stops: 241  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 2316 Std Error: 0.00  
 Seq primer: -28m13 rev2 from Amersham  
 High quality sequence stop: 155.  
 Location/Qualifiers

FEATURES  
 source  
 1..245  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1280499"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:363796"  
 /sex="male"  
 /tissue\_type="retina"  
 /dev\_stage="55 year old"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares retina Nb24HR"  
 /note="Organ: eye; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTACCAATCTGAAGTGGGCGCGCGCGCTTTTATTTTATTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). The retina was obtained from a 55 year old  
 Caucasian and total cellular poly(A)+ RNA was extracted 6  
 hrs after their removal. The retina RNA was kindly  
 provided by Roderick R. McInnes M.D. Ph.D. from the  
 University of Toronto. Library constructed by Bento  
 Soares and M.Fatima Bonaudo. "

ORIGIN  
 Query Match 100.0%; Score 73; DB 9; Length 245;  
 Best Local Similarity 100.0%; Pred. No. 0.0058;  
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTTATTTT 60  
 |||  
 DB 180 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTTATTTT 121  
 |||  
 QY 61 ATTTATTTTTTTT 73  
 |||  
 DB 120 ATTTATTTTTTTT 108  
 |||

RESULT 6  
 D57391/c 284 bp mRNA linear EST 28-AUG-1995  
 LOCUS HMD299H07A Clontech human aorta polyA+ mRNA (#6572) Homo sapiens  
 DEFINITION CDNA clone GEN-299H07 3', mRNA sequence.  
 ACCESSION D57391  
 VERSION D57391.1 GI:964013  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 284)  
 Fujisawa, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, N.,  
 Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,  
 Takachi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,  
 Maekawa, H., Shin, S. and Nakamura, Y.  
 Fujisawa et al. (1995)  
 TITLE Unpublished (1995)  
 JOURNAL Contact: Tautomu Fujiwara  
 COMMENT Otsuka GEN Research Institute  
 Otsuka Pharmaceutical Co., Ltd  
 463-10 Kagasuno Kawachi-cho, Tokushima, Tokushima, 771-01 Japan  
 Tel: 0886-65-2888  
 Fax: 0886-37-1035.

FEATURES  
 source  
 1..284  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="GEN-299H07"  
 /clone\_1ib="Clontech human aorta polyA+ mRNA (#6572)"  
 /location/Qualifiers

ORIGIN  
 Query Match 100.0%; Score 73; DB 14; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 0.0053;  
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTTATTTT 60  
 |||  
 DB 182 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTTATTTT 123  
 |||  
 QY 61 ATTTATTTTTTTT 73  
 |||  
 DB 122 ATTTATTTTTTTT 110  
 |||

RESULT 7  
 BM955729 291 bp mRNA linear EST 30-SEP-2002  
 LOCUS EST10664 HEV PCR-select Homo sapiens CDNA clone HEV1046 similar to  
 DEFINITION protooncogene c-fos, mRNA sequence.  
 ACCESSION BM955729  
 VERSION BM955729.1 GI:23345960  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 291)  
 Palmeri, D., Zhou, F.-R., Rosen, S.D. and Hemmerich, S.  
 Gene expression profiling of peripheral lymph node addressin+ high  
 endothelial venule cells from human tonsil: implications in  
 lymphocyte recirculation and inflammation

JOURNAL Unpublished (2002)  
 COMMENT Contact: Rosen SD  
 Department of Anatomy  
 University of California at San Francisco  
 HSW-1320, 513 Parnassus Ave., San Francisco, CA 94143-0452, USA  
 Tel: 415 476 1579  
 Fax: 415 476 4845  
 Email: sd@itsa.ucsf.edu  
 Seq primer: M13 reverse.  
 Location/Qualifiers  
 1..291  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HEV#1046"  
 /cell\_type="high endothelial"  
 /clone\_1ib="HEV PCR-select"  
 /note="Organ: tonsil; Vector: pCRIT; Site 1: EcoRI;  
 Site 2: EcoRI; High endothelial cells (HEC) were isolated  
 from human tonsils using magnetic beads derivatized with  
 MECA-79 antibody specific to the peripheral lymph node  
 addressin. CDNA was prepared from these cells using  
 Cap-Finder methodology, then cDNA prepared from tonsillar  
 lymphocytes and from human umbilical vein endothelial  
 cells were subtracted from the HEC cDNA, followed by  
 normalization through selective PCR amplification."

ORIGIN  
 Query Match 100.0%; Score 73; DB 12; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 0.0052;  
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTTATTTT 60  
 |||  
 DB 97 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTTATTTT 156  
 |||  
 QY 61 ATTTATTTTTTTT 73  
 |||  
 DB 157 ATTTATTTTTTTT 169  
 |||

RESULT 8  
 BF436565/c 331 bp mRNA linear EST 29-NOV-2000  
 LOCUS 7p15f03.x1 NCI CGAP\_Br22 Homo sapiens CDNA clone IWAGB:3645845 3',  
 DEFINITION mRNA sequence.  
 ACCESSION BF436565  
 VERSION BF436565.1 GI:11448880  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 331)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL Contact: Robert Strusberg, Ph.D.  
 Email: cgsbbs-romail.nih.gov  
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.  
 Emmerit-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 308.  
 Location/Qualifiers  
 1..331  
 /organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_image="3645845"  
/tissue\_type="invasive ductal carcinoma, 3 pooled samples"  
/lab\_host="DH10B (TI-phage resistant)"  
/clone\_lib="NCI CGAP Br22"  
/note="Organ: breast; Vector: PCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.5 Kb. Constructed by Life  
Technologies."

## ORIGIN

Query Match 100.0%; Score 73; DB 10; Length 331;  
Best Local Similarity 100.0%; Pred. No. 0.0048;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTATTTATTTATTAAGATGATTCGATATTTATTTT 60  
|||  
Db 187 AACGTTTATGCTGTTTATTTATTTATTAAGATGATTCGATATTTATTTT 128

QY 61 ATTTATTTT 73  
|||  
Db 127 ATTTATTTT 115

RESULT 9  
BP752720/c 334 bp mRNA linear EST 10-JAN-2001

LOCUS RC4-BN0408-271100-013-f09 BN0408 Homo sapiens CDNA, mRNA sequence.  
DEFINITION BP752720  
ACCESSION BP752720.1 GI:12079396

VERSION BP752720.1 GI:12079396  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 334)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,  
Brunetein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

COMMENT Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
20202663  
10737800

CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC4&t2=RC4-BN0408-  
271100-013-f09&t3=2000-11-27&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 29  
High quality sequence stop: 334.  
Location/Qualifiers

FEATURES  
source  
1..334  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="BN0408"  
/note="Organ: breast-normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 73; DB 10; Length 334;  
Best Local Similarity 100.0%; Pred. No. 0.0048;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTATTTATTTATTAAGATGATTCGATATTTATTTT 60  
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Db 102 AACGTTTATGCTGTTTATTTATTTATTAAGATGATTCGATATTTATTTT 43

QY 61 ATTTATTTT 73  
|||  
Db 42 ATTTATTTT 30

## RESULT 10

AM347336 337 bp mRNA linear EST 09-JUL-2000  
LOCUS AM347336  
DEFINITION 30736 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.  
ACCESSION AM347336  
VERSION AM347336.1 GI:6844983

KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
Sus scrofa

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE 1 (bases 1 to 337)  
Valienkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,  
Valier, J., Wise, T., Rohrer, G.A., Perlee, G., Sultana, R.,  
Quackenbush, J. and Keefe, J.W.

COMMENT Porcine gene discovery by normalized cDNA-library sequencing and  
EST cluster assembly  
Mamm. Genome 13 (8), 475-478 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
12213789  
12226715

CONTACT: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 20  
and -mismatch 12 options.  
PCR primers  
FORWARD: AGGAAACGATGATGACCAT  
BACKWARD: GTTTCGCCGACGACGACG  
Plate: 9 row: L column: 21  
Seq primer: ATTTAGGTGACACTATG.

FEATURES  
source  
1..337  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 1Pig"  
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;  
library made from pooled tissue from day 11, 13, 15, 20,  
and 30 embryos."

## ORIGIN

Query Match 100.0%; Score 73; DB 10; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.0048;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTATTTATTTATTAAGATGATTCGATATTTATTTT 60  
|||  
Db 165 AACGTTTATGCTGTTTATTTATTTATTAAGATGATTCGATATTTATTTT 224

QY 61 ATTTATTTTTTTT 73  
 DB 225 ATTTATTTTTTTT 237  
 RESULT 11  
 LOCUS CA771107/c 338 bp mRNA linear EST 03-DEC-2002  
 DEFINITION 1070h05.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6131937 3',  
 mRNA sequence.  
 ACCESSION CA771107  
 VERSION CA771107.1 GI:26008149  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 338)  
 AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
 Lendshak,I., Scaerce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
 Hillier,L., Marra,M., Page,D., Wylie,T., Martin,J., Blistein,A.,  
 Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J.,  
 Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R.,  
 Williams,T., Jackson,Y. and Bowers,Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Harvard University, Howard Hughes Medical Institute  
 Endocrine Pancreas Consortium  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Hiroshi Inoue  
 (hinoue@im.wustl.edu)  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 313.  
 FEATURES  
 Source  
 1..338  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6131937"  
 /tissue\_type="Purified pancreatic islet"  
 /lab\_host="DH10B"  
 /clone\_1lb="HR85 islet"  
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
 NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
 Size-selected on agarose gel. Average insert size ~1kb. 5'  
 XhoI site was destroyed after directional cloning.  
 Amplified once. Contact information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permutt Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110, E-mail: hinoue@im.wustl.edu, Tel:  
 314-362-1916, Fax: 314-747-2692."

RESULT 12  
 LOCUS CA434443/c 339 bp mRNA linear EST 08-NOV-2002  
 DEFINITION UI-H-DIO-ary-h-05-0-UI.s1 NCI CGAP D10 Homo sapiens cDNA clone  
 UI-H-DIO-ary-h-05-0-UI 3', mRNA sequence.  
 ACCESSION CA434443  
 VERSION CA434443.1 GI:24798863  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 339)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strauberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 The following repetitive elements were found in this cDNA  
 sequence: 122-148, >AT rich#low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.  
 FEATURES  
 Source  
 1..339  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-DIO-ary-h-05-0-UI"  
 /tissue\_type="Lung Focal Fibrosis"  
 /dev\_stage="Adult"  
 /lab\_host="NCI CGAP D10"  
 /note="Organ: Lung; Vector: pRT3-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
 NCI CGAP D10 is a cDNA library containing the following  
 tissue(s): A pool of Lung Focal Fibrosis. The library was  
 constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into pRT3-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (drr)18 tail. The sequence tag for this library is  
 ATACGGCGTC.  
 TAG\_TISSUE=Lung with fibrosis  
 TAG\_LIB=UI-H-DIO  
 TAG\_SEQ=ATACGGCGTC"

ORIGIN  
 Query Match 100.0%; Score 73; DB 14; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 0.0047;  
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AACGTTTATGCTTTTATTTATTTATTAAGATGATTCGAGATTTATTTT 60  
 DB 194 AACGTTTATGCTTTTATTTATTTATTAAGATGATTCGAGATTTATTTT 135  
 QY 61 ATTTATTTTTTTT 73  
 DB 134 ATTTATTTTTTTT 122  
 RESULT 13



CB068539/c	CB068539	350 bp	mRNA	linear	EST 21-JAN-2003							
LOCUS	1829d11.x1	HB85 islet	Homo sapiens	cDNA clone	IMAGE:6553965 3'							
DEFINITION	mRNA sequence.											
ACCESSION	CB068539											
VERSION	CB068539.1	GI:27813059										
KEYWORDS	EST.											
SOURCE	Homo sapiens											
ORGANISM	Homo sapiens (human)											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.											
AUTHORS	Melton,D., Brown,J., Kenty,G., Permut,A., Lee,C., Kaestner,K., Lemishka,I., Scarce,M., Bresnell,J., Gradwohl,G., Clifton,S., Hillier,L., Marray,M., Page,D., Wylie,T., Martin,T., Blissett,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarashvili,R., Williams,T., Jackson,Y. and Bowers,Y.											
TITLE	Endocrine Pancreas Consortium											
JOURNAL	Unpublished (2000)											
COMMENT	Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue											

**FEATURES**

**SOURCE**

Location/Qualifiers  
1. .350

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6553965"  
 /tissue\_type="Purified pancreatic islet"  
 /lab\_host="DH10B"  
 /clone\_1lb="HR85 islet"  
 /note="Oxgan: Pancreas; Vector: pbluescript SK(-); Site 1:  
 Not; Site 2: XhoI; cDNA made by oligo-dT priming.  
 Size-selected on agarose gel. Average insert size ~1kb. 5'  
 XhoI site was destroyed after directional cloning.  
 Amplified once. Contact Information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permut Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110, E-mail: hinoue@umc.wustl.edu, Tel:  
 314-362-1816, Fax: 314-747-2692."

## ORIGIN

Query Match	100.0%;	Score 73;	DB 14;	Length 350;
Best Local Similarity	100.0%;	Pred. No. 0.0046;		
Matches 73; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	AACGTTTAAATGCGTTTAAATTAATTAATTAAGAAGATTCACAGATATTATAATTTT	60
Db	195	AACGTTTAAATGCGTTTAAATTAATTAATTAAGAAGATTCACAGATATTATAATTTT	136
Qy	61	ATTTAATTTTTT	73
Db	135	ATTTAATTTTTT	123

RESULT 14	
AM021706	
LOCUS	351 bp mRNA linear EST 13-SEP-1999
DEFINITION	dfz7g10.y1 Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:	2284450 5', mRNA sequence.
ACCESSION	AM021706

VERSION	AM021706.1	GI:5875236
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 351)	
AUTHORS	Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.	
TITLE	Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening	
JOURNAL	Genomics 23, 42-50 (1994)	
MEDLINE	95130111	
PUBMED	7829101	
COMMENT	Contact: Morton, C. C.	

**FEATURES**  
**source**

Location/Qualifiers  
1. .351

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:248450"
/tissue_type="cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_1fb="Morton Petal Cochlea"
/notes="Organ: ear; Vector: plasmid SK-; Site_1: EcoRI;
Site_2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
unidirectionally. Primer: Oligo dt. Petal cochlea, normal.
37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
XR Vector. Library constructed by N. Robertson, C. Morton.
-5' adaptor sequence: 5' GAATCGCACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

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## ORIGIN

Query Match	100.0%	Score 73	DB 9	Length 351
Best Local Similarity	100.0%	Pred. No. 0.0046		
Matches 73	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	AACGTTTATGCTTTTAAATTTATTTATTAAGATGCTCAGATTTATATTTT	60
	275	AAACGTTTATGCTTTTAAATTTATTTATTAAGATGCTCAGATTTATATTTT	334
Db	275	AAACGTTTATGCTTTTAAATTTATTTATTAAGATGCTCAGATTTATATTTT	334
QY	61	ATTTATTTT	73
	335	ATTTATTTT	347
Db	335	ATTTATTTT	347

[illegible]

REFERENCE  
AUTHORS

1 (bases 1 to 352)

Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,  
Lemshka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Bliscain, A.,  
Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,  
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelshvili, R.,  
Williams, T., Jackson, Y. and Bowers, Y.

TITLE  
JOURNAL  
COMMENT

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138

Tel: 617-495-1812  
Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hinoue@im.wustl.edu)

Seq primer: -40RP from Gibco  
High quality sequence stop: 322.

FEATURES  
source

Location/Qualifiers

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1..352
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:553989"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_id="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permut lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
```

## ORIGIN

Query Match 100.0%; Score 73; DB 14; Length 352;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATCTCAGATATTATATTTT 60
    |||||||
Db 197 AACGTTTATGCTGTTTAAATTTATTTATTTATTAAGATGATCTCAGATATTATATTTT 138

Oy 61 ATTTTATTTT 73
    |||||||
Db 137 ATTTTATTTT 125
    |||||||
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Search completed: October 14, 2004, 18:41:36  
Job time : 1922 secs